

GenCore version 5.1.3
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY									
Result N.	Query Match Score	Sequence	Length	Database	Description				
1	76	100.0	214	3	B1052878	B1052878	B1052878	B1052878	B1052878
2	60	100.0	214	3	B105475	B105475	B105475	B105475	B105475
3	60	100.0	215	3	B267843	B267843	B267843	B267843	B267843
4	60	100.0	234	2	B275462	B275462	B275462	B275462	B275462
5	60	100.0	275	2	B8644124	B8644124	B8644124	B8644124	B8644124
6	60	100.0	279	2	B1804323	B1804323	B1804323	B1804323	B1804323
7	60	100.0	190	19	AW845219	CM0-C10	AW845219	CM0-C10	AW845219
8	60	100.0	294	3	B1050529	CM2-CM2	B1050529	CM2-CM2	B1050529
9	60	100.0	297	12	B1869430	QV0-ET1	B1869430	QV0-ET1	B1869430
10	60	100.0	412	10	B267845	K-EST00	B267845	K-EST00	B267845
11	60	100.0	358	14	B0328387	CM0-C10	B0328387	CM0-C10	B0328387
12	60	100.0	364	14	B0366118	PM1-C10	B0366118	PM1-C10	B0366118
13	60	100.0	404	14	B105715	RC0-H10	B105715	RC0-H10	B105715
14	60	100.0	413	14	B267845	FCT-GNA	B267845	FCT-GNA	B267845
15	60	100.0	413	14	B0366118	PM1-C10	B0366118	PM1-C10	B0366118
16	60	100.0	417	10	AW97331	RC2-BNA	AW97331	RC2-BNA	AW97331
17	60	100.0	454	14	B105053	CM2-GNA	B105053	CM2-GNA	B105053
18	60	100.0	460	14	B0366118	PM1-C10	B0366118	PM1-C10	B0366118
19	60	100.0	469	9	A1834242	RC0-H10	A1834242	RC0-H10	A1834242
20	50	100.0	481	14	B1056715	RC5-GNA	B1056715	RC5-GNA	B1056715
21	50	100.0	482	14	B267845	FCT-GNA	B267845	FCT-GNA	B267845
22	50	100.0	483	14	B0366118	PM1-C10	B0366118	PM1-C10	B0366118
23	60	100.0	484	10	BE314916	H1056715	BE314916	H1056715	BE314916
24	60	100.0	484	14	B0366118	PM1-C10	B0366118	PM1-C10	B0366118
25	60	100.0	490	13	B0366118	PM1-C10	B0366118	PM1-C10	B0366118
26	60	100.0	496	14	B105715	RC0-H10	B105715	RC0-H10	B105715
27	60	100.0	507	14	B0366118	PM1-C10	B0366118	PM1-C10	B0366118
28	60	100.0	540	14	B0366118	PM1-C10	B0366118	PM1-C10	B0366118
29	60	100.0	546	14	B0366118	PM1-C10	B0366118	PM1-C10	B0366118
30	60	100.0	541	14	B0366118	PM1-C10	B0366118	PM1-C10	B0366118
31	50	100.0	553	14	B0366118	PM1-C10	B0366118	PM1-C10	B0366118
32	60	100.0	564	12	B0366118	PM1-C10	B0366118	PM1-C10	B0366118
33	60	100.0	572	14	B105715	RC0-H10	B105715	RC0-H10	B105715
34	60	100.0	574	10	BE294933	RC2-BNA	BE294933	RC2-BNA	BE294933
35	60	100.0	583	14	B0366118	PM1-C10	B0366118	PM1-C10	B0366118
36	60	100.0	590	14	B0366118	PM1-C10	B0366118	PM1-C10	B0366118
37	60	100.0	593	14	B0366118	PM1-C10	B0366118	PM1-C10	B0366118
38	60	100.0	593	14	B0366118	PM1-C10	B0366118	PM1-C10	B0366118
39	60	100.0	608	14	B105715	RC0-H10	B105715	RC0-H10	B105715
40	60	100.0	615	14	B0366118	PM1-C10	B0366118	PM1-C10	B0366118
41	60	100.0	621	12	B0366118	PM1-C10	B0366118	PM1-C10	B0366118
42	60	100.0	632	14	B0366118	PM1-C10	B0366118	PM1-C10	B0366118
43	60	100.0	633	10	AW993854	RC3-BNA	AW993854	RC3-BNA	AW993854
44	60	100.0	642	10	HF301419	RC2-BNA	HF301419	RC2-BNA	HF301419
45	60	100.0	697	9	AU141534	AU141534	AU141534	AU141534	AU141534

Hrusztein, A., de Oliveira, P.S., Bucher, P., Jongenelis, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and Simpson, A.J.

TITLE Short run sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

COMMENT Laboratory of Cancer Genetics
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This sequence was derived from the FAPESP/LIRP Human Cancer Genome Project. This entry can be seen in the following URL:
<http://www.ludwig.org.br/bsc/sets/actinu2.p1?u=RC5&t2=RC5-GNC281-240101-021-021-021-H01517-2001-02-01&c4=1>

Seq. primer: puc 18 forward

High quality sequence step: 214.

Location/Qualifiers

1. Site_1: Small; A mini-library was made by cloning vector puc18. This sequence was derived from the FAPESP/LIRP Human Cancer Genome Project. This entry can be seen in the following URL:
<http://www.ludwig.org.br/bsc/sets/actinu2.p1?u=RC5&t2=RC5-GNC281-240101-021-021-021-H01517-2001-02-01&c4=1>

Note: "Organ: placenta normal; Vector: puc18; Site_1: small products derived from QRESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
67 a 36 c 88 q 23 t

FEATURES

SOURCE

1. Site_1: Small; A mini-library was made by cloning vector puc18. This sequence was derived from the FAPESP/LIRP Human Cancer Genome Project. This entry can be seen in the following URL:
<http://www.ludwig.org.br/bsc/sets/actinu2.p1?u=RC5&t2=RC5-GNC281-240101-021-021-021-H01517-2001-02-01&c4=1>

COMMENT

COMMENT

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This sequence was derived from the FAPESP/LIRP Human Cancer Genome Project. This entry can be seen in the following URL:
<http://www.ludwig.org.br/bsc/sets/actinu2.p1?u=RC5&t2=RC5-GNC281-240101-021-021-021-H01517-2001-02-01&c4=1>

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High quality sequence step: 214.

Location/Qualifiers

1. Site_1: Small; A mini-library was made by cloning vector puc18. This sequence was derived from the FAPESP/LIRP Human Cancer Genome Project. This entry can be seen in the following URL:
<http://www.ludwig.org.br/bsc/sets/actinu2.p1?u=RC5&t2=RC5-GNC281-240101-021-021-021-H01517-2001-02-01&c4=1>

FEATURES

SOURCE

1. Site_1: Small; A mini-library was made by cloning vector puc18. This sequence was derived from the FAPESP/LIRP Human Cancer Genome Project. This entry can be seen in the following URL:
<http://www.ludwig.org.br/bsc/sets/actinu2.p1?u=RC5&t2=RC5-GNC281-240101-021-021-021-H01517-2001-02-01&c4=1>

COMMENT

COMMENT

Contact: Simpson A.J.G.
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Tel.: +55-11-2704922
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Email: asimposon@ludwig.org.br
 This sequence was derived from the PAPERS/MICR Human Cancer Genome project. This entry can be seen in the following URL:
http://www.ludwig.org.br/scripts/gethtml2.php?ID=NC56t2_RC5_CNO281-150201-013-A93t3-2001-02-25&t4-1

FEATURES

Source	Location/Qualifiers
1..215	Organism="Homo sapiens"
/db_xref="taxon:9006"	
/clone_id="CN0281"	
/dev_state="Adult"	
/note="Organ: placenta-normal; Vector: purla; Site_1: small	
; Site_2: Small; A mini library was made by cloning	
products derived from ORESTES PCR (U.S. letters patent	
application No. 196,716 - Ludwig Institute for Cancer	
Research) profiles into the pUC 18 vector. Reverse	
transcription of tissue mRNA and cDNA amplification were	
performed under low stringency conditions."	

BASE COUNT

ORIGIN	22 a	34 g	68 t
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Alignment Scores.

Pred. No.:	0.0169	Length:	215
Score:	6.00	Matches:	12
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match.:	100.0%	Holes:	0
DB:	14	Gaps:	0

US-09-856-070-21 {1-12} x RQ467843 (1-215)

QY

1 GluGlutCunArgLeuGluGluGluGlu 12

DB

160 GAGGACTGATcccccccccACATACAGACAG 125

RESULT 4

LOCUS BG754562

DEFINITION 60271013461 NIH-MCC_48 Homo sapiens cDNA clone IMAGE:4846630 5 , mRNA sequence.

ACCESSION BG754562

VERSION BG754562_1

KEYWORDS EST.

ORGANISM Human

COMMENT Contact: Robert Strainsberg, Ph.D.
 Email: rcs@nih.gov

REFERENCE Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

AUTHORS CDNA Library Preparation: Liudong Liu/Ratna Laboratory

JOURNAL CUNA Library Arrayed by: The I.M.A.G.E. Consortium (LJN1.)

COMMENT DNA Sequencing RV: Invitae Genomics, Inc.
 Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov/LLCM187>

FEATURES

Source	Location/Qualifiers
1..234	Organism="Homo sapiens"
/db_xref="taxon:9006"	
/clone="IMAGE:4846630"	
/clone_id="NIH-MCC_48"	
/tissue-type="primary B-cells from tonsils (cell line)"	
/lab-host="OHIO Phage-resistant"	
/note="Organ: B-cells; Vector: pOTB7; Site_1: XbaI;	
Site_2: EcoRI; cDNA made by oligo-dT priming.	

Directionally cloned into EcoRI/XbaI sites using the forward 5' adapter: GGTWGAATTC. Size-selected >500bp for average insert size 1.8kb. Library constructed by Linq Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-*cDNA* synthesis kit (Stratagene) and SuperScript II RT (Life Technologies). Note: this is a NIH-MCC Library."

BASE COUNT

ORIGIN	81 a	36 c	96 q	19 t
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Alignment Scores.

Pred. No.:	0.0191	Length:	234
Score:	6.00	Matches:	12
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-856-070-21 {1-12} x RQ754562 (1-234)

QY

1 GluGlutCunArgLeuGluGluGluGlu 12

DB

103 GAGGACTGATcccccccccACATACAGACAG 138

RESULT 5

LOCUS BM844124

DEFINITION F-US-09-856-070-21 NS13RMGS-18-G03 5 , mRNA Sequence.

ACCESSION BM844124

VERSION BM844124.1

KEYWORDS EST.

SOURCE Human.

ORGANISM Homo sapiens

COMMENT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 215)

AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, S., and Kim, Y.S., Cheung, J.W., Shin, H.Y., Kim, J.M., Park, H.S., Kim, S., and Kim, Y.S.

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Disributed (2002)

COMMENT CGATcat. Kim YS
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 Tel.: +82-42-860-4470
 Fax: +82-42-860-4499
 Email: Yongsung@mail.kribb.re.kr
 Plate: 38 row: G column: 03
 High quality sequence stop: 275,
 location/Qualifiers
 1..275
 /organism="Homo sapiens"
 /db_xref="taxon:9006"
 /clone="NS13RMGS-18-G03"
 /clone_id="NS13RMGS-18-G03"
 /tissue-type="myeloma"
 /cell-line="KMS-5",
 /lab-host="top10F"

COMMENT Site_1: EcoRI; Site_2: NotI; The poly A+ RNA was phosphorylated with bacterial alkaline phosphatase (BAP) and then decapped mRNA by priming with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA RNA linker including EcoRI 1 site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60 nt. The cDNA vector was circularized with E. coli RNA ligase after digestion of vector which site is also included in vector. An RNA strand converted to a DNA strand by Okayama Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli

US-09-856-070-21 (1-12) x AW845119 (1-281)	QY	1	GlutathioneMetLeuArgLeuValAspTyrlGluGln	12
DB	176	GAGGATGAACTGGCGCCAGCAATAGGGAG	211	
RESULT 8	BI050028.c	BI050328.g	294 hg	mRNA Linear
LOCUS	CMC_GN004_0001_01	676-208	GN0294	Human Reference cDNA
DEFINITION	CMC_GN004			EST 15-JUN-2001
ACCESSION	BI050028			EF000002
VERSION	BI050028.1			
KEYWORDS	EST.			
SOURCE	human			
ORGANISM	Homo sapiens			
Eukaryota				
Metazoa				
Chordata				
Craniata				
Vertebrata				
Euvertebrata				
Mammalia				
Primates				
Hominoidea				
Homidae				
Human				
REFERENCE	1	(bases 1 to 294)		
AUTHORS	Dias Neto,E., Garcia Correa,R., Verjovsky-Almada,S., Briones,M.R., Nasal,M.A., da Silva,W.Jr., Zago,M.A., Bordin,C., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsuoka,A., Baiia,G.S., Simpson,D.H., Brunstein,A., de Oliveira,P.S., Bicher,P., Jorgaezel,C.V., Chare,M.J., Soares,F., Arntzeni,P.R., Pais,I., F., de Souza,S., and Simpson,A.J.			
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags			
JOURNAL	Proc Natl Acad Sci U S A	q7 (7),	3491-3496	(2000)
MEDLINE	2020663			
COMMENT	Contact: Simpson A.J.G.			
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	Brazil			
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	Fax: +55-11-277001			
	Email: asimpson@ludwig.org.br			
	This sequence was derived from the FAPESP/Ludwig Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gtgbnum2pvt1?gtgbnum2=020101-676-008&3=2001-01-02&t14=1)			
	Seq primer: puc 18 forward			
	High quality sequence start: 17			
	High quality sequence stop: 294.			
FEATURES	Localization/Localizers			
	1..294			
source	/organism="Homo sapiens"			
	/db_xref="HGNC:0006"			
	/clone_id="GN0294"			
	/dev_stage="Adult"			
	/note="Organ: placenta_normal; Vector: puc18; Site_1: Small site_2: Small; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."			
BASE COUNT	34 a 114 c 56 g 90 t			
ORIGIN				
Alignment Scores:				
Pred. No.:	0.0266			
Score:	60.00			
Percent Similarity:	100.00%			
Best Local Similarity:	100.00%			
Query Match:	100.00%			
DB:	13			
	length: 294			
	Matches: 12			
	conservation: 0			
	Mismatches: 0			
	indels: 0			
	Gaps: 0			
US-09-856-070-21 (1-12) x BI050028 (1-294)	QY	1	GlutathioneMetLeuArgLeuValAspTyrlGluGln	12
DB	213	GAGGATGAACTGGCGCCAGCAATAGGGAG	211	EF000002
				17g

VERSION HMW27086.1 GI:19183495
 SOURCE FST
 ORGANISM Homo sapiens
 KEYWORDS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; primates; Catarrhini; Hominidae; Homo.
 REFERENCE ATTH-PS
 AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.T., Cheong, J.E., Sonn, H.Y., Kim, J.M., Park, H.S., Kim, S., and Kim, Y.S.
 TITLE 21C Frontier Korean EST Project, 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
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 Tel.: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yonsun@kribb.re.kr
 Plate: 4 row: 6 column: 09
 High quality sequence step: 312.

FEATURES source
 site_1: 1..312
 site_2: 1..312
 site_3: "Human_sapiens"
 /db_xref="Exon", 600,*
 /clone_id="S9SN601..44..C09"
 /clone_id="S9SN601"
 /seq_id="M"

FEATURES source
 site_1: "Asciates"
 /cell_line="Epithelial"
 /lab_host="top10F"
 /note="organ: Stomach; Vector: pME18-FLX; site_1: XbaI; site_2: XbaI; the poly(A) RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with tRNA RNA linker including Sfi I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using Sfi I oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified with Sfi I and debrayed by electroporation method."
 The cDNA libraries constructed by this method are full-length enriched cDNA library.
 BASE COUNT 108 a 60 c 110 g 34 t
 ORIGIN

Alignment Scores:
 Pred. No.: 0.0353
 Score: 60.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 14
 BASE COUNT 112 a 74 c 130 q 42 t
 ORIGIN

Alignment Scores:
 Pred. No.: 0.0353
 Score: 60.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 14
 BASE COUNT 112 a 74 c 130 q 42 t
 ORIGIN

RESULT 12
 LOCUS HQ368118
 DEFINITION pM3-ON0516-094501-010-d10 GRN0516_Homo_sapiens_CDNA_mRNA_Sequence
 ACCESSION HQ368118
 VERSION HQ368118.1
 KEYWORDS EST, Human
 SOURCE BQ368118
 ORGANISM Homo sapiens
 KEYWORDS Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Dias, Neto, E., Garcia, Correa, P., Verjovsky-Almeida, S., Britto, M.R., Goldstein, G.H., Carvalho, A.F., Matsukuma, A., Bordin, S., Costa, F.P., Simpson, D.H., Brunstein, A., do Oliveira, P.S., Bucher, P., Joncencet, C.V., de Souza, S.J. and Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 COMMENT Contact: Simpson, A.J.G.
 Laboratoy of Cancer Genetics
 Ludwig Institute for Cancer Research
 Brazil Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel.: 55-11-2704922
 Fax: 55-11-2707061
 Email: asimpon@ludwig.org.br
 This sequence was derived from the PRPFSP/LUDW Human Cancer Genome Project. This entry can be seen in the PRPFSP/LUDW Human Cancer Genome Database at <http://www.ludwig-oncology.org/prpfsp/prpfsp2/PrfPrf2/PrfPrf2.html#648-butgr4-000-10-305t4-1>

FEATURES source
 site_1: small;
 site_2: small; A mini-library was made by cloning products derived from cDNAs PCR (U.S. Letters patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
 BASE COUNT 112 a 74 c 130 q 42 t
 ORIGIN

Alignment Scores:
 Pred. No.: 0.0353
 Score: 60.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 14
 BASE COUNT 112 a 74 c 130 q 42 t
 ORIGIN

RESULT 12
 LOCUS HQ368118
 DEFINITION pM3-ON0516-094501-010-d10 GRN0516_Homo_sapiens_CDNA_mRNA_Sequence
 ACCESSION HQ368118
 VERSION HQ368118.1
 KEYWORDS EST, Human
 SOURCE BQ368118
 ORGANISM Homo sapiens
 KEYWORDS Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Dias, Neto, E., Garcia, Correa, P., Verjovsky-Almeida, S., Britto, M.R., Goldstein, G.H., Carvalho, A.F., Matsukuma, A., Bordin, S., Costa, F.P., Simpson, D.H., Brunstein, A., do Oliveira, P.S., Bucher, P., Joncencet, C.V., de Souza, S.J. and Simpson, A.J.

RESULT 11
 LOCUS HQ323837
 DEFINITION CM0-C0095_301000-648-h05_C1005_Homo_sapiens_CDNA_mRNA_Sequence
 ACCESSION HQ323837
 VERSION HQ323837..1
 KEYWORDS EST, Human
 SOURCE Homo sapiens
 ORGANISM Homo sapiens

COMMENT
FEATURES
SON
BASE COU
ORIGIN
Alignment
Pred.: No
Score:
Percent:
Best Loc:
Query Ma
DB:
TS-09-85
29
Nb 25
RESULT 1
BM44711
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
EGAN
REFERENCE
AUTHOR
TITLE
JOURNAL
COMMENT

This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL:
<http://www.ludwig.org.br/scripts/gethtml2.pl?1-MR4&t2-MR4-KT0047>
 16050-003-10&t3-001-05-16&t4-1)

clone.lib-S4SNU1

clone.lib-S4SNU1

Sex="M"

A tissue type="Stomach"

Cell type="SNU-1"

Lab host="Top10F"

Note-(organ): Stomach; Vector: pTZ19RPL; Site_1: EcoRI;

Site_2: NotI; The poly(A) RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA RNA linker including EcoRI 1 site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from cDNA-H-selected mRNA by priming with dG-tailed vector. The dG-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayana-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10^E by electroporation method.

The cDNA libraries constructed by this method are full-length enriched cDNA library.

BASE COUNT 127 a 83 c 141 q 53 t

ORIGIN

Alignment Scores:

Pred. No.:	0.042	Length:	404
Score:	60.00	Matches:	12
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:		Gaps:	0

US-09-856-070-21 (1-12) x HQ300862 (1-413)

Qy 1 GluculoseMetLeuAsnAspTyroGluGlu 12

Db 189 AGGAGTTATGTTGTTGGCTAGGACTATGAGAG 155

Search completed: January 16, 2003, 21:37:07
 Job time : 1588.77 secs

RESULTS 15

Qy 1 GluculoseMetLeuAsnAspTyroGluGlu 12

Db 273 GAGGAGTTATGTTGTTGGCTAGGACTATGAGAG 308

RESULT 15

ORGANISM HQ300862/c

DEFINITION HQ300862 MR4_KT0047-160501-003-164 Homo sapiens mRNA sequence.

VERSION HQ300862.1 GI:20816384

KEYWORDS EST 16-MAY-2002

SOURCE human

ORGANISM Homo sapiens

Filoxotida: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 413)

AUTHORS Dias Neto,F., Garcia Correa,R., Verjovski Almeida,S., Briones,M.R., Nardi,M.A., da Silveira,W.Jr., Bordin,S., Costa,F.F., Goldmire,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., de Oliveira,P.S., Bucher,P., Joncene,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,I.F., de Souza,S.J., and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

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